

1 AGCATCTGA GTAATGAGTG GCCTGGGCGG GAGCAGGCGA GGTGGCCGGA GCCGTGTGGA CCAGGAGGAG CGCTTTCAC AGGGCCTGTG GAGGGGGGTG
TCGTAGGACT CATTACTCAG CGGACCGGCG CTCGTCCGCT CCACCGGCCT CGGCACACCT GGTCTCTCTC GCGARAGGTG TCCCGGACAC CTGCCCCACAC
M S G L G R S R R S R V D Q E E R F P Q G L W T G V
101 GCTATGAGAT CCTGCCCCGA AGAGCACTAC TGGGATCTCT TGCTGGGTAC CTGATGTCC TGCARACCA TTGCRACCA TCAGAGCCAG CGCACCTGTG
CGATACTCTA GGRCGGGGT TCTCGTCAAG ACCCTAGGAG AGRACCCATG GACGTACAGG ACGTTTGGT AAAGTTGGT AGTCTGGTC GCGTGGACAC
30 A M R S C P E E Q Y W D P L L G T C M S C K T I C N H Q S Q R T C A
201 CAGCCTTCTG CAGGTCACTC AGCTGCCCGA AGGAGCAAGG CRACTTCTAT GACCATCTCC TGGGGACTG CATCAGCTGT GCCTCCATCT GTGCACAGCA
GTCCGAGAC GTCCAGTCAG TCGACGGGT TCTCGTCTCC GTTCAAGATA CTGTAGAGG ACTCCCTGAC GTAGTCGACA CGGAGGTAGA CACTGTGCT
64 A F C R S L S C R K E Q G K F Y D H L L R D C I S C A S I C G Q H
301 CCCTAGACAA TGTGATRACT TCTGTAGAA CRACTCAGG AGCCAGTGA ACCTTCCACC AGAGCTCAGG AGACAGCCGA GTGAGNAGT TGAACACAT
GGGATTCGTT ACACGTATGA AGACACTCTT GTTCGAGTCC TCGGCTCACT TGGNAGTGG TCTCGAGTCC TCTGAGCTC ACCTCTTCA ACTTTGTGA
97 P K Q C A Y F C E N K L R S P V N L P P E L R R Q R S G E V E N N
401 TCAGACACT CGGGRAGTA CCAAGGATG GAGCACAGG GCTCAGAAGC AAGTCCAGCT CTCCCGGGG TGAAGCTGAG TGCAGATCAG GTGSCCCTG
AGTCTGTGA GGCCTTCCAT GGTCTCTAAC CTGTGTCTC CGAGTCTTCG TTCAGTCTGA GAGGGCCCG ACTTCGACTC ACCTCTAGTC CACCGGAC
130 S D N S G R Y Q G L E H R G S E A S P A L P G L K L S A D Q V A L V
501 TCTACAGCAC GCTGGGGCTG TGCCTGTGTG CCGTCTCTG CTGCTTCTG GTGGCGTGG CTGCTTCTT CAGAAGAGG GGGATCCCT GCTCTGCCA
AGATGTCTG CGACCCCGAG ACGACACAC ACGAGGAGAC GAGCAGGAC CACCGCCACC GGACGAGGA GTTCTTCTCC CCCTAGGA CGAGACGGT
164 Y S T L G L C L C A V L C C F L V A V A C F L K K R G D P C S C Q
601 GCCCGCTCA AGCCCCGTC AAGTCCGGC CAGTCTTCC CAGGATCAG CGATGAAGC CGGCAGCCCT GTGAGCACAT CCCCGAGCC AGTGAGACC
CGGGCGAGT TCGGGGGCAG TTTCAGGCGG GTTCAGAAGG GTCCTAGTC GCTACCTTCG GCGTCCGGA CATCTGTGA GGGGCTCGG TCACCTCTG
197 P R S R P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T
701 TGCAGCTTCT GCTTCCCTGA GTGCAGGGG CCGAGGCGAG AGAGCCAGT CAGGCTGGG ACCCCCGACC CCACTTGTG TGAAGGTGG GGGTCCACA
ACGTGAGAG CAGAGGACT CAGTCCCGC GGTGCGTCC TCTGCGTCA GTGCGACCC TGGGGGTGG GGTGAACAGG ACCTCCACC CCCAGGTGT
230 C S F C F P E C R A P T Q E S A V T P G T P D P T C A G R W G C H T
801 CCAGGACCAC AGTCTGCRG CCTTGCCAC ACATCCACA CAGTGGCTT GCAATGTGT GTGTGCCCTG CCGAGAGGG GGCACAGGT CATTAATGG
GGTCTGTG TCAAGACGTC GAGGGGTG TGTAGGTCT GTACCGGA CCGTACACA CACAGGAGG GGTCTCCCG CCGGTCCAC GTATTACCC
264 R T T V L Q P C P H I P D S G L G I V C V P A Q E G G P G A O

FIG. 1A

901 GGTGAGGAG GGAAGGAGG AGGAGAGAG ATGGAGAGG GGGAGAGAG AAAGAGAGGT GGGAGAGGG GAGAGAGATA TGAGAGAGA GAGCAGAGG
 CCAGTCCCTC CTTTCCTCC TCCCTCTCTC TACCTCTCT TCTCTCTCA CCCCCTCCC CTCTCTCTAT ACTCTCTCT CTCTCTCTC
 1001 AGGCAGNAAG GAGAGNAAC AGGAGAGACA GAGAGGAGA GAGAGAGAGA GGCAGAGAGA GACAGAGGG AGAGAGGCA GAGAGGAAA GAGGAGAGA
 TCCGTCTTC CCTCTTTG TCTCTCTGT CTCTCTCTCT CTCTCTCTCT CCCTCTCTCT CTGTCTCCC TTCTCTCGT CTCTCCCTT CTCTCTCTCT
 1101 AGGAGAGAGA CAGGAGAGA AGGAGAGAGG CAGAGAGAGA GAGAGGAGA GGCAGAGAGA CAGAGAGGGA GAGAGGACA GAGAGAGATA
 TCCCTCTCT GTCCGTCTCT TCCCTCTCTC GTCTCTCTCT CTCTCTCTCT CCGTCTCTCT GTCTCTCTCT CTCTCTCTCT CTCTCTCTAT
 1201 GAGCAGGAGG TCGGGGCACT CTGAGTCCCA GTTCCAGTG CAGCTGTAGG TCGTCATCAC CTACCCACAC GTCCATATAA GTCTCTGTG CTCTCTCTCA
 CTCGTCTCTC AGCCCGTGA GACTCAGGT CAAGGTCTAC GTCCACATCC AGCAGTAGTG GATTGGTGTG CACGTATTTT CAGGAGCAG GACGACGAGT
 1301 CAGCCCCGA GAGCCCTCC TCCTGGAGAA TAAACCTTT GGCAGCTGCC CTTCCTCAAA AAAAAAAAAA AAAAAA
 GTCGGGGCT CTCGGGAGG AGGACCTCTT ATTTGGAA CCGTCGACGG GAAGAGTTT TTTTITTTT TTTTTT

FIG. 1B

HTACI(265)	10	20	30	40	50
HTACI	M S C L C R S R R G G R S R V Q Q E E R F P Q G L W T G V A M R S C P E E Q Y W D P L L G T C M S C				
	60	70	80	90	100
	M S C L C R S R R G G R S R V Q Q E E R F P Q G L W T G V A M R S C P E E Q Y W D P L L G T C M S C				
HTACI(265)	110	120	130	140	150
HTACI	K T I C N H Q S Q R T C A A F C R S L S C R K E Q G K F Y D H L L R D C I S C A S I C G Q H P K Q C				
	160	170	180	190	200
	K T I C N H Q S Q R T C A A F C R S L S C R K E Q G K F Y D H L L R D C I S C A S I C G Q H P K Q C				
HTACI(265)	210	220	230	240	250
HTACI	A Y F C E N K L R S P V N L P P E L R R Q R S G E V E N N S D N S G R Y Q G L E H R G S E A S P A L				
	260	270	280	290	300
	A Y F C E N K L R S P V N L P P E L R R Q R S G E V E N N S D N S G R Y Q G L E H R G S E A S P A L				
HTACI(265)	310	320	330	340	350
HTACI	P G L K L S A D Q V A L V Y S T L G L C L C A V L C C F L V A V A C F L K K R G D P C S C Q P R S R				
	360	370	380	390	400
	P G L K L S A D Q V A L V Y S T L G L C L C A V L C C F L V A V A C F L K K R G D P C S C Q P R S R				
HTACI(265)	410	420	430	440	450
HTACI	P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T C S F C F P E C R A P T Q E S A V T P G T				
	460	470	480	490	500
	P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T C S F C F P E C R A P T Q E S A V T P G T				
HTACI(265)	510	520	530	540	550
HTACI	P D P T C A G R T A P P R E G Z				
	560	570	580	590	600
	P D P T C A G R T A P P R E G Z				

FIG. 1C

1 ARGAGCTCAA CTTAGAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG ACACAGACAG CCCCCTAAG ACCCCAGAA GCAGGGGAAG
TTCTGAGTTT GAATCTTTGA ACTTAATCTA CACCATAGT TTAGGAATGC ACGGCGCTTC TGTGTCTGTC GGGGSCATTC TTGGGTGCTT CGTCCGCTTC
101 TTCATTGTC TCACATTCT AGCTGCTCTT GCTGCATTG CTTCTGGAATT CTCTGAGAGA TATTACTTGT CCTTCAGGC TGTCTCTTCT GTAGCTCCCT
AAGTAACAG AGTTGTAAGA TCGACGAGAA CGACGTAAAC GAGACCTTAA GACATCTCT ATAATGARCA GGAAGTCCG ACAGAAAGA CATCGAGGGA
201 TGTCTCTTT TTGTGATCAT GTTCAGATG GCTGGGAGT GCTCCCAAAA TGAATATTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACCTCGAT
ACAAAAGAAA AACACTAGTA CAACGCTAC CGACCCGTCA CGAGGGTTTT ACTTATAAA CTGTCAAACA ACGTACGAAC GTATGGAACA GTTGAAGCTA
1 Me tLeuGlnMet AlaGlyGlnC ysSerGlnAs nGluTyrPhe AspSerLeul euHisAlaCy sileProCys GlnL uArgC
301 GTTCTTCTAA TACTCTCTCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT CAGTGAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG
CAAGNAGATT ATGAGGAGGA GATTGTACAG TCGCAATAC ATTACGTTCA CACTGGTTAA GTCACCTTCC TTGCTTAGCG TAAGAGACCT GGACAAACCC
29 ysSerSerAs nThrProPro LeuThrCysG lnArgTyrCy sAsnAlaSer valThrAsnS erValLysG1 yThrAsnAla lleLeuTrrpT hrCysLeuG1
401 ACTGAGCTTA ATAATTTCTT TGSCAGTTT CGTGCTAATG TTTTGTCTAA GGAAGATAAG CTCTGAACCA CTAAAGGAGG AGTTTAAAAA CACAGGATCA
TGACTCGAAT TATTAAAGAA ACCGTCAAAA GCACGATTAC AAAAACGATT CCTTCTATTG GAGACTTGGT AATTTCCTGC TCRAATTTTT GTGTCTCTAGT
62 yLeuSerLeu llelleSerL euAlaValPh eValLeuMet PheLeuLeuA rgLysileSe rSerGluPro LeuLysAspG luPheLysAs nThrGlySer
501 GGTCTCTCG GCATGGCTAA CATTGACCTG GAAAGAGCA GGACTGGTGA TGAATTTATT CTTCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT
CCAGAGGACC CGTACCGATT GTAACCTGGAC CTTTCTCTCGT CCTGACCACT ACTTTAATAA GAAGGCTCTC CGGAGCTCAT GTGCCACCTT CTTACGTGGA
95 GlyLeuLeuG lyMetalaAs nileAspLeu GluLysSera rgThrGlyAs pGluillelle LeuProArgG lyLeuGluTy rThrValGlu GluCysThrC
601 GTGAAGACTG CATCAAGAGC AAACCGAAG TCGACTCTGA CCATTGCTTT CCACTCCCAG CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC
CACTTCTGAC GTAGTTCTCG TTTGGCTTCC AGCTGAGACT GGTAAACGAA GGTGAGGGTC GATACCTCCT TCCGCGTTGG TAAGAACAGT .GGTCTTTTG
129 ysGluAspCy sileLysSer LysProLysV alAspSerAs pHisCysPhe ProLeuProA laMetGluG1 uGlyAlaThr lleLeuValT hrThrLysTh
701 GAATGACTAT TGCAAGAGCC TGCCAGCTGC TTTGAGTGTCT ACGGAGATAG AGAATCAAT TTCTGCTAGG TAATTAAACA TTTCGACTCG AGCAGTGCCA
CTTACTGATA ACGTCTCGG ACGGTGACG AAACCTCACGA TGCCCTCTATC TCTTTAGTTA AAGACGATCC ATTAATTGGT AAAGCTGAGC TCGTCACGGT
162 rAsnAspTy r CysLysSerL euProAlaAl aLeuSerAla ThrGluilleG lulySerIl eSerAlaArg OC+
801 CTTTAAAAAT CTTTGTCTCAG ATAGATGAT GTGTCAGATC TCTTTAGGAT GACTGTATTT TTCACTTGGC GATACAGCTT TTTGTCTCTT AACTGTGGAA
GAATTTTTTA GAACACAGTC TTATCTACTA CACAGTCTAG AGAATCCCTA CTGACATARA AAGTCAACGG CTATGTGCGA AAACAGGAGA TTGACACCTT
901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAACTTC CTGTTTCA TGATTAAGT CTTTTTTTTT CCTGA
TGAGAAATAC AATCTATATA AAGAGATCCA ATGACAACCC TCGAATTACC ATCTTTGAAG GAACCAAGT ACTAATTTCA GAAAAAATAA GGACT

FIG. 2

1 ATGGATGACT CCACAGAAAG GGAGCAGTCA CGCCTTACTT CTGCGCTTAA GAAAGAGAA GAAATGAAC TGAGGAGTG TGTTCCATC CTCACAGGA
TACCTACTGA GGTGTCTTTC CCTCGTCACT GCGGAATGAA GAAGGGAAT CTTTCTCTT CTTTACTTTG ACTTCTCAC ACAGAGGTAG GAGGTGCTT
1 M D D S T E R E Q S R L T S C L K K R E E M K L K E C V S I L P R K
101 AGGAAAGCCC CTCTGTCCGA TCCTCCNAAG ACGGAAGCT GCTGGCTGCA ACCTTGCTGC TGGCACTGCT GTCTTCTGTC CTCACGGTGG TGCTTTCTTA
TCTTTCCGG GAGACAGCT AGGAGTTTC TGCTTTTCA CGACCGACGT TGGACGACG ACOGTGACGA CAGAACGACG GAGTGCCACC ACAGAAAGAT
35 E S P S V R S S K D G K L L A A T L L L A L L S C C L T V V S F Y
201 CCAGGTGGCC GCGCTGCAAG GGGACCTGCG CAGCTCCGG GCAGAGCTGC AGGCCACCA CGCGAGAA GTCGCCAGC GAGCAGGAGC CCCCAGGCC
GGTCCACCG GCGGACGTTT CCTGGACCG GTCCGAGGCC CGTCTGACG TCCCGTGGT GCGCTCTTC GACGGTCTC CTCGCTCTCG GGGGTTCGG
68 Q V A A L Q G D L A S L R A E L Q G H A E K L P A G A G A P K A
301 GGCTTGAGG AAGCTCCAGC TGTACCGCG GGAAGTAA TCTTGNACC ACCAGCTCCA GGAGAGGCA ACTCCAGTCA GAACAGAGA AATAAGGCTG
CCGACCTCC TTGAGGTGCG ACAGTGGCG CCTGACTTTT AGAAGCTGG TGGTCGAGGT CCTCTCOGT TGAGGTCACT CTTGTCTCT TTAATGCTC
102 G L E E A P A V T A G L K I F E P P A P G E G N S S Q N S R N K R A
401 CCGTTCGGG TCCAGAGAA ACAGTCACTC AAGCTGCTT GCAGACAGTG AARACCAAC TATACAAA GGATCTTACA CATTTGTTCC
GGCAAGTCCC AGTCTCTT TGTCACTGAG TTCTGACGAA CGTTCAGTAA CGTCTGCTAC TTGTGGTGG ATATGTTTTT CCTAGATGT GTARACAAGG
135 V Q G P E E T V T Q D C L Q L I A D S E T P T I Q K G S Y T F V P
501 ATGCTTCTC AGCTTTTAAA GGGGAAGTGC CCTAGAAGAA AAGAGANTA AATATTGGT CAAAGAACT GGTACTTTT TTATATATGG TCAGTTTAA
TACGAGAGG TCGAATTTT CCGCTTCAGG GATCTCTCT TTTCTCTTAT TTTATAACCA GTTTCTTTGA CCAATGAAGA AATATATACC AGTCCAAAT
168 W L L S F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L
601 TATACTGATA AGACCTACGC CATGGGACAT CTATTCAGA GGAGAGAGT CCAATGCTTT GGGGATGAAT TGAGTCTGGT GACTTGTGT CGATGTATTC
ATATGACTAT TCTGGATGCG GTACCCCTGA GATTAAGTCT CTTCTTCCA GGTACAGAAA CCCCTACTTA ACTCAGACCA CTGAACAAA GCTACATAG
201 Y T D K T Y A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q
701 AATATATGCC TGAACACTA CCAATATAT CTTCTATTTC AGCTGGCATT GCMAACTGG AAGAGGAGA TGAATCCAA CTTGCATAC CAAGAAA
TTTATACGG ACTTGTGAT GGGTATTAA GGAGATAG TCGACCGTAA CGTTTGACC TTCTCTCTCT ACTTGAGTT GAACGTATG GTTCTCTTT
235 N M P E T L P N N S C Y S A G I A K L E E G D E L Q L A I P R E N
801 TGCACATA TCACTGGATG GAGTGTGAC ATTTTGTGT GCATGAAC TGCTGTA
ACGTGTTTAT AGTGACCTAC CTCTACAGTG TAAAAACCA CGTAAGTTTG ACGACACT
268 A Q I S L D G D V T F F G A L K L L O

FIG. 3

1 GGTACGAGGC TTCTTAGAGG GACTGGAACC TAATTTCTCT GAGGCTGAGG GAGGCTGAGG GGTCTCAGAG CACGCTGGC CCACGACGG AGTCCACAGG
CAATGCTCCG AAGGATCTCC CTGACTTGG ATTAAGAGGA CTCGCATCC CTCCCACCTC CCAGAGTTCC GTTGGACCG GGTGCTGCC TCACGGTCTCT

101 GCACTAACAG TACCCTTAGC TTGCTTTCTT CCTCCCTCCT TTATTTCTTC AGTTCCCTTT TTAATTTCTC TTGGTAAACA ACCTTCTTCC CTTCGTGCACC
CGTGATGTTC ATGGGAATCG AACGAAGGA GGAGGGAGGA AATATAAAG TTCAAGGAAA AATAAAGAG AACCATTTGT TGGAGAGG GRACACGTGG

201 ACTGCCCGTA CCTTACCCG CCCGCCACC TCCTTGCTAC CCACTCTTG AACACACAGC TGTGGCAGG GTCCACAGT CATGCCAGCC TCATCTCCTT
TGACGGGCAT GGGATGGGC GGGGCGGTGG AGGACGATG GGTGAGAAC TTGCTGTGCG ACAACCGTCC CAGGGGTGCA GTACGCTCG AGTAGAGGAA
M P A S S P F

301 TCITGCTAGC CCCRAAGG CCTCCAGGCA ACATGGGGG CCAAGTCAGA GAGCCGGCAC TCTCAGTTGC CCTCTGGTTG AGTTGGGGG CAGCTCTGGG
AGNACGATCG GGGGTTTCCG GAGGTCCGT TGTACCCCCC GGTCTAGTCT CTGCGCCGTG AGAGTCAACG GGAGACCAAC TCACCCCCC GTCCGACACC
8 L L A P K G P P G N M G G P V R E P A L S V A L W L S W G A A L G

401 GGCCGTGGCT TGTGCCANG CTCTGCTGAC CCAACAAACA GAGCTGCAGA GCTCAGGAG GCTCAGGAGG GGACAGGAGG CCCTCCCCAG
CCGGACCCGA ACACGGTACC GAGACGACTG GGTGTTTGT CTGACGCTCT CGAGTCTCTC TCCTCACTCG CCCGACGTCC CCTGTCTTCC GGGGAGGCTC
41 A V A C A M A L L T Q Q T E L Q S L R R E V S R L Q G T G G P S Q

501 AATGGGAAG GGTATCCCTG GCAGAGTCTC CCGAGGAGA GTTCCGATGC CTEGAAGCC TGGAGATG TGGAGATG CCGGAAGG CCGGAAGG AGAGAGTGC
TTACCCCTTC CCATGGGAC GGTCTCAGG GGCCTGCTCT CAGGCTAGG GGACCTTCGG ACCCTCTTAC CCCTCTCTAG GGCCTTTTCC TCTGCTCAGG
74 N G E G Y P W Q S L P E Q S S D A L E A W E N G E R S R K R R A V L

601 TCACCCAAA ACAGAGAG CAGCACTCTG TCCTGCACCT GGTCCCAT TACGCCACCT CCAAGGATGA CTCGATGTG ACAGAGTGA TGTGCAACC
AGTGGGTTT TGTCTTCTC GTCGTGAGAC AGGACGTGGA CCAAGGGTAA TTGGGGTGA GGTCTCTACT GAGGTACAC TGTCTCCACT ACACGTTGG
108 T Q K Q K K Q H S V L H L V P I N A T S K D D S D V T E V M W Q P

701 AGCTCTTAGG CTTGGGAGG CCTACAGGC CCAAGCATAT GTGTCCGAA TCCAGGATGC TGGAGTTTAT CTGCTGTATA GCCAGTCTT GTTTCAGAC
TCGRGATCC GCACCCCTCT CCGATGTCCG GGTCTCTATA CCAAGGCTT AGGTCTCTAG ACCTCAATA GACGACATAT CCGTCCAGGA CAAAGTTCTG
141 A L R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L F Q D

801 GTGACTTTCA CCATGGGTCA GTGGTGTCT CAGAGAGGC AAGGAAGGCA GGAGACTCTA TTCGATGTA TAAGAGTAT GCCCTCCAC CCGACCCGGG
CACTGAAAGT GGTACCCAGT CCACACAGA GCTCTTCCG TTCTTCCGT CCTCTGAGT AAGGTACAT ATTCTTATA CCGGAGGTG GGCCTGGCCC
174 V T F T M G Q V V S R E G Q G R Q E T L F R C I R S M P S H P D R A

901 CTTACACAG CTGCTATAGC GCAGGTGTCT TCAATTTACA CCAAGGGGAT ATTCTGAGT TCATAATTC CCGGGCAAGG GCGAATCTA ACCTCTCTCC
GGATGTTGTC GAGCATATCG CGTCCACAGA AGTAAATGT GGTCCCCCTA TRAGACTCAC AGTATTAAG GGGCCGTTCC CGCTTTGAAT TGGAGAGAGG
208 Y N S C Y S A G V F H L H Q G D I L S V I I P R A R A K L N L S P

FIG. 4A

1001 ACATGGAAAC TTCCTGGGT TTGTGAACCT GTGATTGCT TATRAAAGT GGCTCCACG TTGGAGACC AGGGTGGTA CATACTGGAG ACAGCCAAGA
 TGTAACCTGG AAGGCCCA AACACTTTGA CACTACACA ATATTTTCA CGAGGGTGG AACCTTCTGG TCCACCCAT GTATGACCTC TGTGGTTCT
 241 H G T F L G F V K L Q
 1101 GCTGATATA TAAAGGAG GATATGCA GATATCTCTG GATTGGCTC CCGTTCTC ACTTTTCCCT TTTCATTCCC ACCCCCTAGA
 CGACTCATAT ATTCTCTC CTTACACCT CCTGTCTCC GTAGAAGAC CCAACCGAG GGCRAAGAG TGAAGAAGGA AAGTAAGG TGGGGATCT
 1201 CTTGATTTT ACGGATATCT TGCTTCTGTT CCGCATGGAG CTCGAATTC TTGCTGTGT GTAGTGAAG GGGGGGGAC GGGGGCCAGG CATTTGTCAG
 GAACATAA TGCCTATAGA ACGAGACAA GGGGTACCTC GAGCTTARG AACGCACACA CATCTACTCC CCGCCCCCTG CCGGGGGTCC GTAACAAGTC
 1301 ACCTGGTGG GGGCCACTGG AAGCATCCAG AACAGCACCA CCATCTTA
 TGGACCAGCC CCGGGTGACC TTCTAGGTC TTGCTGGGT GGTAGAT

FIG. 4B

TACIs

agcatcctgagtaATGAGTGGCCTGGGCCGGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGG
AGGAGCGCtGGTCACTCAGCTGCCGCAAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGAC
TGCATCAGCTGTGCCCTCCATCTGTGGACAGCACCCCTAAGCAATGTGCATACTTCTGTGAGAACAA
GCTCAGGAGCCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGGAGTGGAGAAGTTGAAAACA
ATTGAGACAACCTCGGGAAGGTACCAAGGATTGGAGCACAGAGGCTCAGAAGCAAGTCCAGCTCTC
CCGGGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGGCTCTGCCTGTG
TGCCGTCTCTGCTGCTTCTTGGTGGCGGTGGCCTGCTTCTCAAGAAGAGGGGGGATCCCTGCT
CCTGCCAGCCCCGCTCAAGGCCCCGCTCAAAGTCCGGCCAAGTCTTCCCAGGATCACGCGATGGAA
GCCGGCAGCCCCGTGAGCACATCCCCGAGCCAGTGGAGACCTGCAGCTTCTGCTTCCCTGAGTG
CAGGGCGCCCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCCGACCCCACTTGTGCTGGAAGGT
GGGGGTGCCACACCAGGACCACAGTCTTGCAGCCTTGCCACACATCCCAGACAGTGGCCTTGGC
ATTGTGTGTGTGCCGTGCCAGGAGGGGGGCCAGGTGCATAAatgggggtcagggaggggaaagga
ggagggagagagatggagaggaggggagagagaaagagaggtggggagaggggagagagatatga
ggagagagagacagaggaggcagaaaggagagaaacagaggagacagagagggagagagagaca
gagggagagagagacagaggggaagagaggcagagagggaaagaggcagagaaggaaagagacag
gcagagaaggagagaggcagagagggagagaggcagagagggagagaggcagagagacagagagg
gagagagggacagagagagatagagcaggaggtcggggcactctgagtcccagttcccagtgag
ctgtagggtcgatcacctaaccacacgtgcaataaagtccctcgctgctgctcacagcccc
gagagccccctcctcctggagaataaaacctttggcagctgcccttcctcaaaaaaaaaaaaaaaaa
aaaa

Fig. 5A

TACIs :

MSGLGRSRRGGRSRVDQEERWSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSP
VNLPPELRRQRSGEVENNSDMSGYQGLEHRGSEASPALFGLKLSADQVALVYSTLGLCLCAVLC
CFLVAVACFLKKRGDFCSCQPRSRPRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAFT
QESAVTPGTPDPTCAGRWGCHTRTTVLQPCPHIPDSGLGIVCVPAQEGGPG

Fig. 5B

human BR3:

cgtcggcaccATGAGGCGAGGGCCCCGGAGCCTGCGGGGCAGGGACGCGCCAGCCCCACGCCCT
GCGTCCCGGCCGAGTGCTTCGACCTGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACG
CCGCGGCCGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAGCCGCAGGAGTC
GGTGGGCGCGGGGGCCGGCGAGGCGGCGCTGCCCCTGCCCGGGCTGCTCTTTGGCGCCCCCGCGC
TGCTGGGCCTGGCACTGGTCCTGGCGCTGGTCCTGGTGGGTCTGGTGAGCTGGAGGCGGCGACAG
CGGCGGCTTCGCGGCGCGTCCTCCGCAGAGGCCCCGACGGAGACAAGGACGCCCCAGAGCCCCT
GGACAAGGTCATCATTCTGTCTCCGGGAATCTCTGATGCCACAGCTCCTGCCTGGCCTCCTCCTG
GGGAAGACCCAGGAACCAACCCACCTGGCCACAGTGTCCCTGTGCCAGCCACAGAGCTGGGCTCC
ACTGAACTGGTGACCACCAAGACGGCCGGCCCTGAGCAACAATAGcagggagccggcaggaggtg
gccccctgccc

Fig. 6A

BR3:

MRRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGA
GAGEAALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPLDKV
IILSPGISDATAPAWPPPGEDEPGTTPPGHSVPVPATELGSTELVTTKTAGPEQQ

Fig. 6B

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 15 = 33.3%

FIG. 7A

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

FIG. 7B

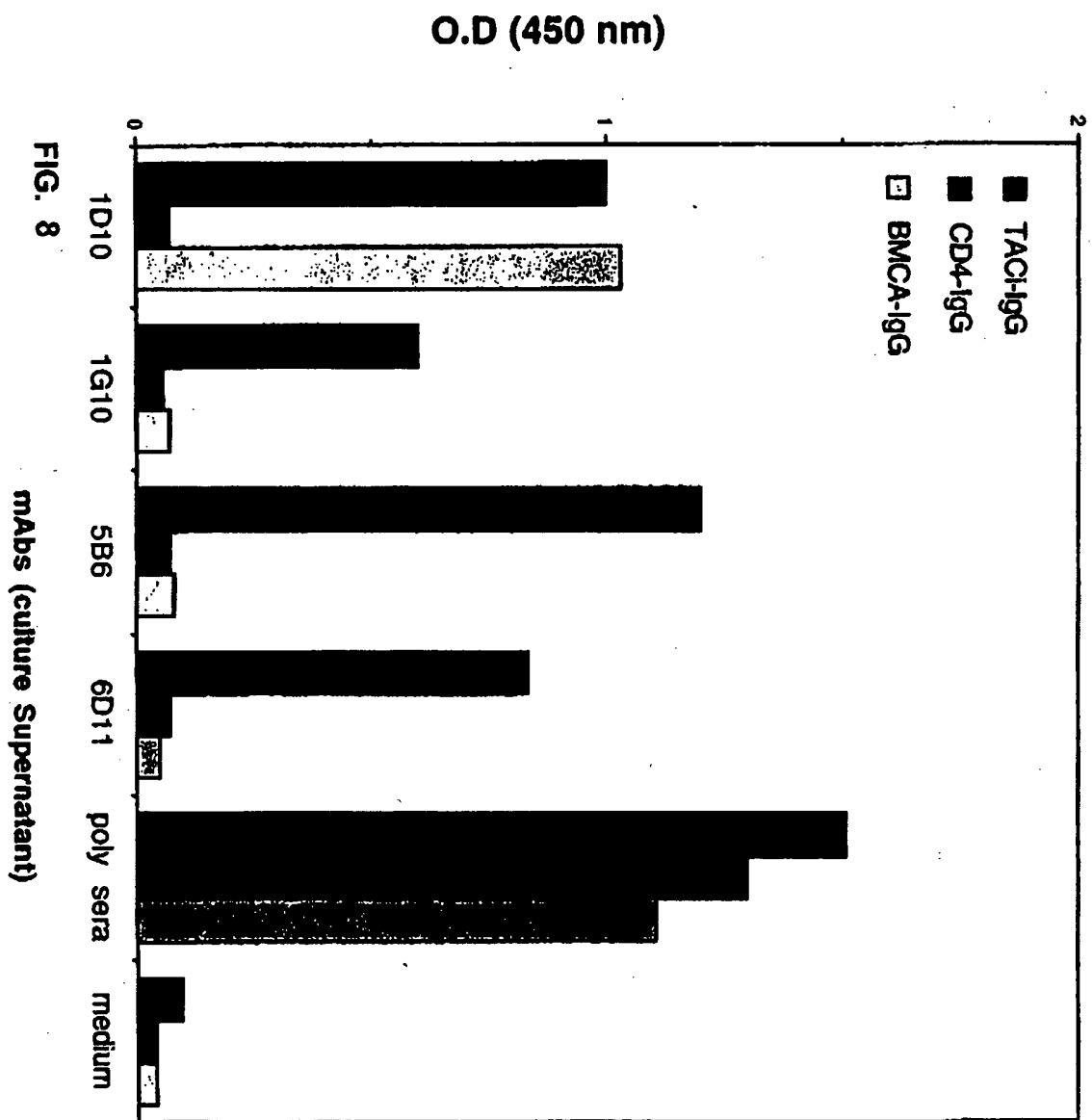


FIG. 8

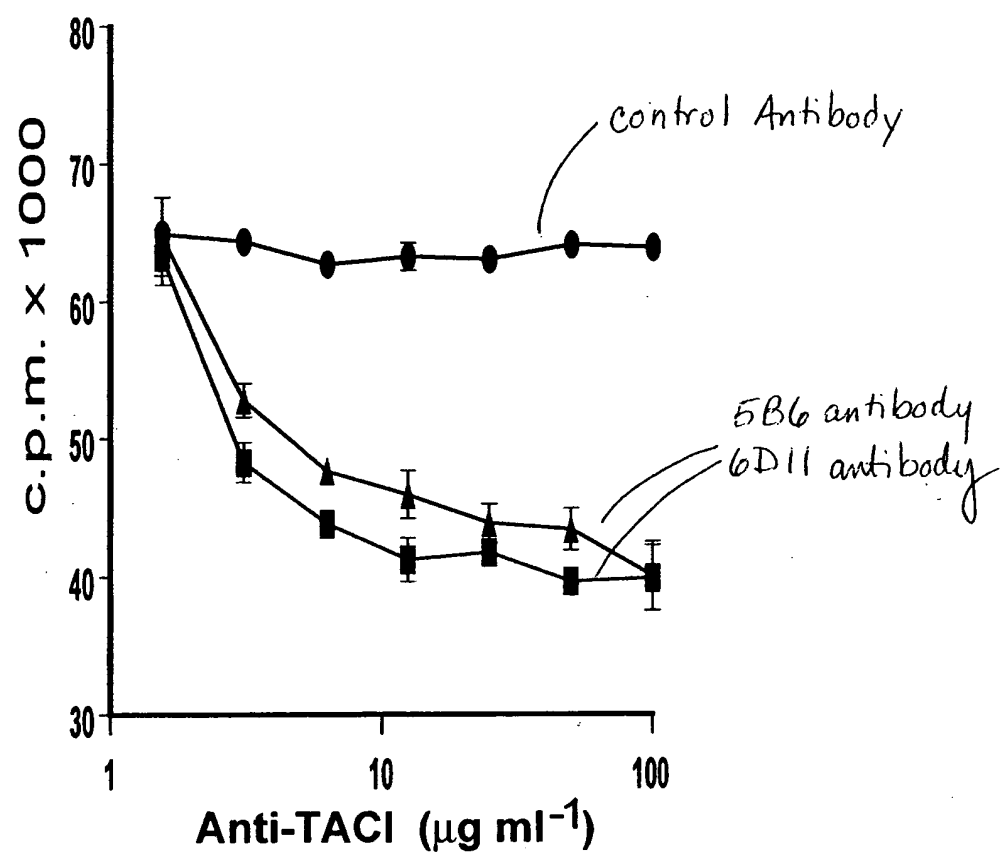


Figure 9

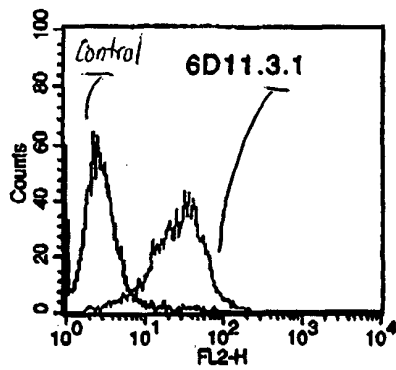
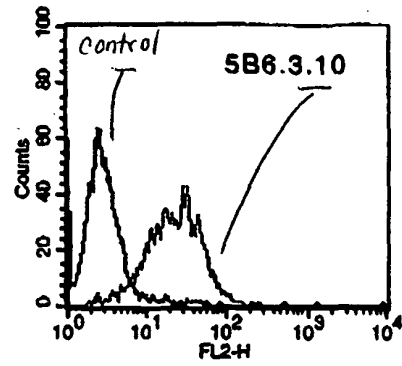
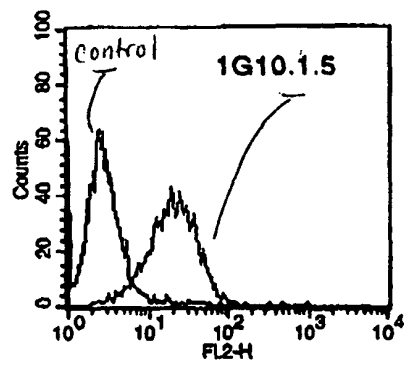


FIG. 10

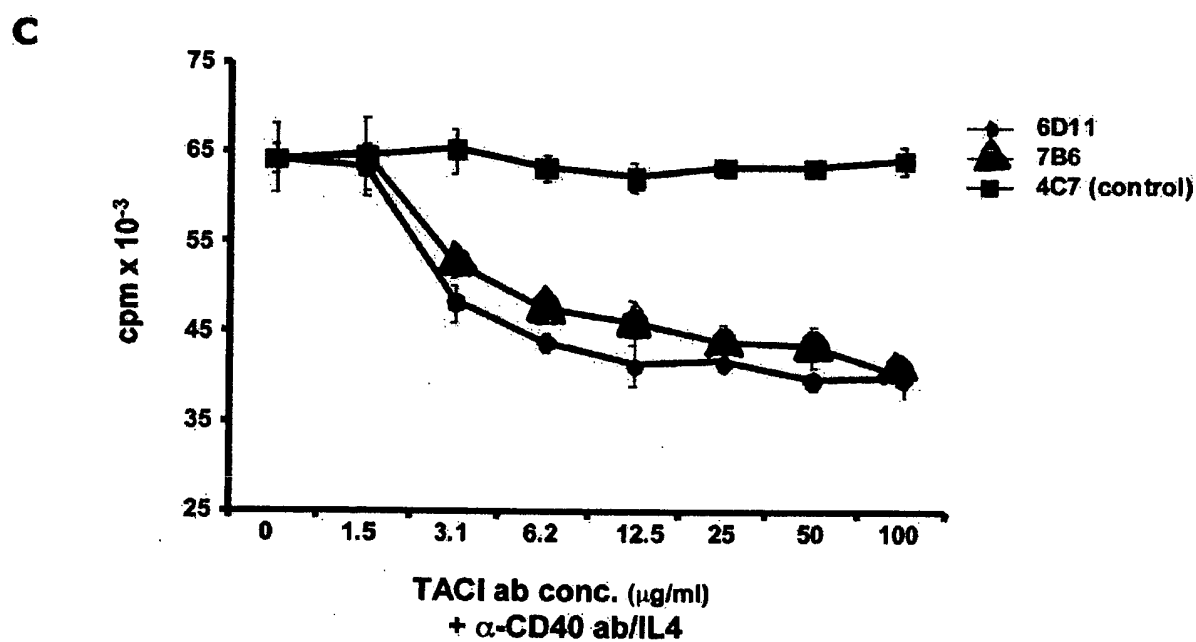
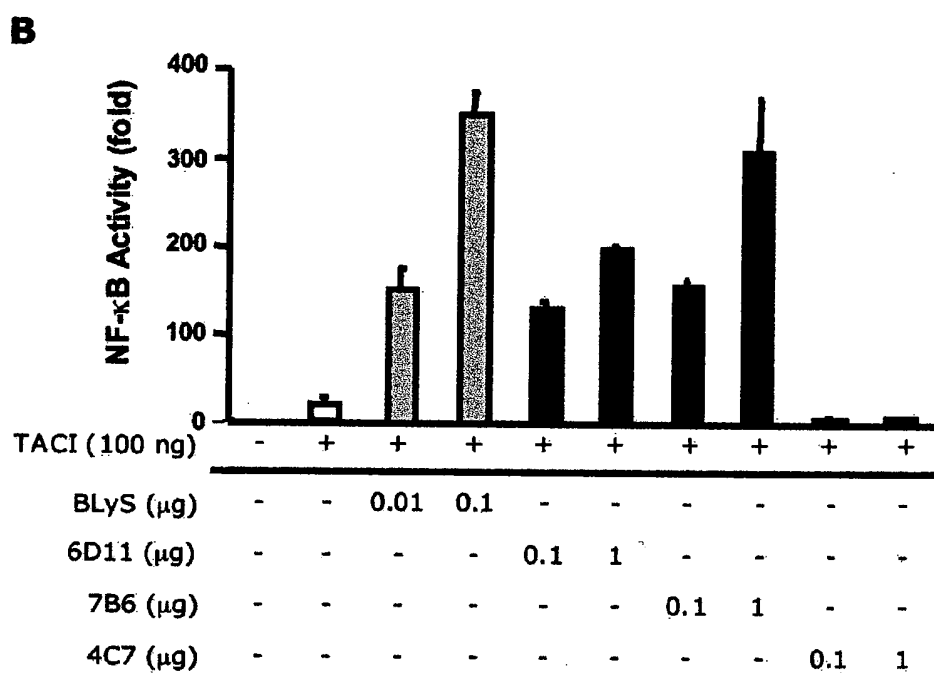
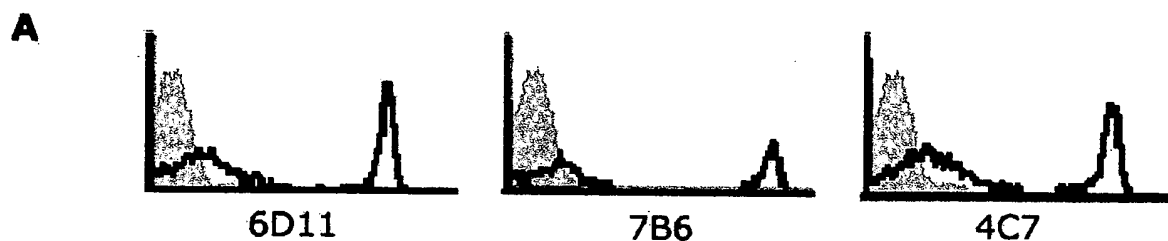


FIG. 11